

SEQUENCE LISTING

<110> Wakamiya, Nobutaka

<120> NOVEL COLLECTIN

<130> 19036/36615

<140>

<141>

<150> PCT/JP98/03328

<151> 1998-07-24

<150> JP 10-11281

<151> 1998-01-23

<160> 29

<170> PatentIn Ver. 2.0

<210> 1

<211> 1595

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (6)..(836)

<400> 1

cagca atg aat ggc ttt gca tcc ttg ctt cga aga aac caa ttt atc ctc 50
Met Asn Gly Phe Ala Ser Leu Leu Arg Arg Asn Gln Phe Ile Leu
1 5 10 15

ctg gta cta ttt ctt ttg caa att cag agt ctg ggt ctg gat att gat 98
Leu Val Leu Phe Leu Leu Gln Ile Gln Ser Leu Gly Leu Asp Ile Asp
20 25 30

agc cgt cct acc gct gaa gtc tgt gcc aca cac aca att tca cca gga 146
Ser Arg Pro Thr Ala Glu Val Cys Ala Thr His Thr Ile Ser Pro Gly
35 40 45

ccc aaa gga gat gat ggt gaa aaa gga gat cca gga gaa gag gga aag 194
Pro Lys Gly Asp Asp Gly Glu Lys Gly Asp Pro Gly Glu Glu Gly Lys
50 55 60

cat ggc aaa gtg gga cgc atg ggg ccg aaa gga att aaa gga gaa ctg 242
His Gly Lys Val Gly Arg Met Gly Pro Lys Gly Ile Lys Gly Glu Leu
65 70 75

ggg gat atg gga gat cgg ggc aat att ggc aag act ggg ccc att ggg 290
Gly Asp Met Gly Asp Arg Gly Asn Ile Gly Lys Thr Gly Pro Ile Gly
80 85 90 95

aag aag ggt gac aaa ggg gaa aaa ggt ttg ctt gga ata cct gga gaa	338
Lys Lys Gly Asp Lys Gly Glu Lys Gly Leu Leu Gly Ile Pro Gly Glu	
100 105 110	
aaa ggc aaa gca ggt act gtc tgt gat tgt gga aga tac cgg aaa ttt	386
Lys Gly Lys Ala Gly Thr Val Cys Asp Cys Gly Arg Tyr Arg Lys Phe	
115 120 125	
gtt gga caa ctg gat att agt att gcc cgg ctc aag aca tct atg aag	434
Val Gly Gln Leu Asp Ile Ser Ile Ala Arg Leu Lys Thr Ser Met Lys	
130 135 140	
ttt gtc aag aat gtg ata gca ggg att agg gaa act gaa gag aaa ttc	482
Phe Val Lys Asn Val Ile Ala Gly Ile Arg Glu Thr Glu Glu Lys Phe	
145 150 155	
tac tac atc gtg cag gaa gag aag aac tac agg gaa tcc cta acc cac	530
Tyr Tyr Ile Val Gln Glu Glu Lys Asn Tyr Arg Glu Ser Leu Thr His	
160 165 170 175	
tgc agg att cgg ggt gga atg cta gcc atg ccc aag gat gaa gct gcc	578
Cys Arg Ile Arg Gly Gly Met Leu Ala Met Pro Lys Asp Glu Ala Ala	
180 185 190	
aac aca ctc atc gct gac tat gtt gcc aag agt ggc ttc ttt cgg gtg	626
Asn Thr Leu Ile Ala Asp Tyr Val Ala Lys Ser Gly Phe Phe Arg Val	
195 200 205	
ttc att ggc gtg aat gac ctt gaa agg gag gga cag tac atg ttc aca	674
Phe Ile Gly Val Asn Asp Leu Glu Arg Glu Gly Gln Tyr Met Phe Thr	
210 215 220	
gac aac act cca ctg cag aac tat agc aac tgg aat gag ggg gaa ccc	722
Asp Asn Thr Pro Leu Gln Asn Tyr Ser Asn Trp Asn Glu Gly Glu Pro	
225 230 235	
agc gac ccc tat ggt cat gag gac tgt gtg gag atg ctg agc tct ggc	770
Ser Asp Pro Tyr Gly His Glu Asp Cys Val Glu Met Leu Ser Ser Gly	
240 245 250 255	
aga tgg aat gac aca gag tgc cat ctt acc atg tac ttt gtc tgt gag	818
Arg Trp Asn Asp Thr Glu Cys His Leu Thr Met Tyr Phe Val Cys Glu	
260 265 270	
ttc atc aag aag aaa aag taacttccct catcctacgt atttgctatt	866
Phe Ile Lys Lys Lys Lys	
275	
ttcctgtgac cgtcattaca gttattgtta tccatccttt ttttctgat tgtactacat	926
ttgatctgag tcaacatagc tagaaaatgc taaactgagg tatggagcct ccatcatcat	986
gctcttttgt gatgatcttc atattttcac acatgggtatg ttattgaccc aataactcgc	1046
caggttacat ggggtcttgag agagaatttt aattactaat tgtgcacgag atagttgggt	1106

gtctatatgt caaatgagtt gttctcttgg tatttgctct accatctctc cctagagcac 1166
tctgtgtcta tcccagtga taatttccca gtttactggg gatgattagg aagggtgttg 1226
atggttaggc taacctgccc tggcccaaag ccagacatgt acaagggctt tctgtgagca 1286
atgataagat ctttgaatcc aagatgccca gatgttttac cagtcacacc ctatggccat 1346
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aacggagcc 1595

<210> 2
<211> 277
<212> PRT
<213> Homo sapiens

<400> 2
Met Asn Gly Phe Ala Ser Leu Leu Arg Arg Asn Gln Phe Ile Leu Leu
1 5 10 15
Val Leu Phe Leu Leu Gln Ile Gln Ser Leu Gly Leu Asp Ile Asp Ser
20 25 30
Arg Pro Thr Ala Glu Val Cys Ala Thr His Thr Ile Ser Pro Gly Pro
35 40 45
Lys Gly Asp Asp Gly Glu Lys Gly Asp Pro Gly Glu Glu Gly Lys His
50 55 60
Gly Lys Val Gly Arg Met Gly Pro Lys Gly Ile Lys Gly Glu Leu Gly
65 70 75 80
Asp Met Gly Asp Arg Gly Asn Ile Gly Lys Thr Gly Pro Ile Gly Lys
85 90 95
Lys Gly Asp Lys Gly Glu Lys Gly Leu Leu Gly Ile Pro Gly Glu Lys
100 105 110
Gly Lys Ala Gly Thr Val Cys Asp Cys Gly Arg Tyr Arg Lys Phe Val
115 120 125
Gly Gln Leu Asp Ile Ser Ile Ala Arg Leu Lys Thr Ser Met Lys Phe
130 135 140
Val Lys Asn Val Ile Ala Gly Ile Arg Glu Thr Glu Glu Lys Phe Tyr
145 150 155 160

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Tyr Ile Val Gln Glu Glu Lys Asn Tyr Arg Glu Ser Leu Thr His Cys
165 170 175

Arg Ile Arg Gly Gly Met Leu Ala Met Pro Lys Asp Glu Ala Ala Asn
180 185 190

Thr Leu Ile Ala Asp Tyr Val Ala Lys Ser Gly Phe Phe Arg Val Phe
195 200 205

Ile Gly Val Asn Asp Leu Glu Arg Glu Gly Gln Tyr Met Phe Thr Asp
210 215 220

Asn Thr Pro Leu Gln Asn Tyr Ser Asn Trp Asn Glu Gly Glu Pro Ser
225 230 235 240

Asp Pro Tyr Gly His Glu Asp Cys Val Glu Met Leu Ser Ser Gly Arg
245 250 255

Trp Asn Asp Thr Glu Cys His Leu Thr Met Tyr Phe Val Cys Glu Phe
260 265 270

Ile Lys Lys Lys Lys
275

<210> 3
<211> 27
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Consensus
sequence of collectins which were reported
heretofore

<400> 3
Glu Lys Cys Val Glu Met Tyr Thr Asp Gly Lys Trp Asn Asp Arg Asn
1 5 10 15

Cys Leu Gln Ser Arg Leu Ala Ile Cys Glu Phe
20 25

<210> 4
<211> 14
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Pre-sequence
of an Insert

<400> 4
gaattcggca cgag

<210> 5
<211> 24
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: M13 Universal
Primer Sequence for Sequencing

<400> 5
cgacgttgta aaacgacggc cagt

24

<210> 6
<211> 17
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: M13 Reverse
Primer Sequence for Sequencing

<400> 6
caggaaacag ctatgac

17

<210> 7
<211> 21
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Sequence of a
Reverse Primer for Screening a Novel Collectin

<400> 7
ttttgatgga ggctccatac c

21

<210> 8
<211> 21
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Sequence of a
Forward Primer for Screening a Novel Collectin

<400> 8
ctgccaacac actcatcgct g

21

<210> 9
<211> 24
<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Sequence of a
lambda gt11 Reverse Primer for Sequencing

<400> 9

ttgacaccag accaactggt aatg

24

<210> 10

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Sequence of a
lambda gt11 Forward Primer for Sequencing

<400> 10

ggtggcgacg actcctggag cccg

24

<210> 11

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Sequence of a
Synthetic Primer for Sequencing a Novel Collectin

<400> 11

taatggtagc gaccggcgct

20

<210> 12

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Sequence of a
Synthetic Primer for Sequencing a Novel Collectin

<400> 12

aaaccaattt atactcctgg

20

<210> 13

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Sequence of a
Synthetic Primer for Sequencing a Novel Collectin

<400> 13

aatattggca agactgggcc

20

<210> 14

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Sequence of a
Synthetic Primer for Sequencing a Novel Collectin

<400> 14

gatgagtgtg ttggcagcat

20

<210> 15

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Sequence of a
Synthetic Primer for Sequencing a Novel Collectin

<400> 15

gtatcttcca caatcacaga

20

<210> 16

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Sequence of a
Synthetic Primer for Sequencing a Novel Collectin

<400> 16

ttaattcctt tcggcccat

20

<210> 17

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Sequence of a
Synthetic Primer for Sequencing a Novel Collectin

<400> 17
gcaaaagaaa tagtaccagg 20

<210> 18
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Sequence of a
Synthetic Primer for Sequencing a Novel Collectin

<400> 18
catatcaccc agttctcctt 20

<210> 19
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Sequence of a
Synthetic Primer for Sequencing a Novel Collectin

<400> 19
agcagggatt agggaaactg 20

<210> 20
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Sequence of a
Synthetic Primer for Sequencing a Novel Collectin

<400> 20
ctgtgagcgt cattacagtt 20

<210> 21
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Sequence of a
Synthetic Primer for Sequencing a Novel Collectin

<400> 21
ggttgcttat atgtcaaatg 20

<210> 22
<211> 20
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Sequence of a
Synthetic Primer for Sequencing a Novel Collectin

<400> 22
tatggccatg gctatacttg

20

<210> 23
<211> 20
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Sequence of a
Synthetic Primer for Sequencing a Novel Collectin

<400> 23
atcgctgact atgttgccaa

20

<210> 24
<211> 20
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Sequence of a
Synthetic Primer for Sequencing a Novel Collectin

<400> 24
caagtatagc catggccata

20

<210> 25
<211> 20
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Sequence of a
Synthetic Primer for Sequencing a Novel Collectin

<400> 25
aactgtaatg acgctcacag

20

<210> 26
<211> 20
<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Sequence of a
Synthetic Primer for Sequencing a Novel Collectin

<400> 26

catttgacat atgaacaacc

20

<210> 27

<211> 248

<212> PRT

<213> Homo sapiens

<220>

<223> mannan-binding protein (MBP)

<400> 27

Met Ser Leu Phe Pro Ser Leu Pro Leu Leu Leu Leu Ser Met Val Ala
1 5 10 15

Ala Ser Tyr Ser Glu Thr Val Thr Cys Glu Asp Ala Gln Lys Thr Cys
20 25 30

Pro Ala Val Ile Ala Cys Ser Ser Pro Gly Ile Asn Gly Phe Pro Gly
35 40 45

Lys Asp Gly Arg Asp Gly Thr Lys Gly Glu Lys Gly Glu Pro Gly Gln
50 55 60

Gly Leu Arg Gly Leu Gln Gly Pro Pro Gly Lys Leu Gly Pro Pro Gly
65 70 75 80

Asn Pro Gly Pro Ser Gly Ser Pro Gly Pro Lys Gly Gln Lys Gly Asp
85 90 95

Pro Gly Lys Ser Pro Asp Gly Asp Ser Ser Leu Ala Ala Ser Glu Arg
100 105 110

Lys Ala Leu Gln Thr Glu Met Ala Arg Ile Lys Lys Trp Leu Thr Phe
115 120 125

Ser Leu Gly Lys Gln Val Gly Asn Lys Phe Phe Leu Thr Asn Gly Glu
130 135 140

Ile Met Thr Phe Glu Lys Val Lys Ala Leu Cys Val Lys Phe Gln Ala
145 150 155 160

Ser Val Ala Thr Pro Arg Asn Ala Ala Glu Asn Gly Ala Ile Gln Asn
165 170 175

Leu Ile Lys Glu Glu Ala Phe Leu Gly Ile Thr Asp Glu Lys Thr Glu
180 185 190

Gly Gln Phe Val Asp Leu Thr Gly Asn Arg Leu Thr Tyr Thr Asn Trp
195 200 205

Asn Glu Gly Glu Pro Asn Asn Ala Gly Ser Asp Glu Asp Cys Val Leu
210 215 220

Leu Leu Lys Asn Gly Gln Trp Asn Asp Val Pro Cys Ser Thr Ser His
225 230 235 240

Leu Ala Val Cys Glu Phe Pro Ile
245

<210> 28

<211> 248

<212> PRT

<213> Homo sapiens

<220>

<223> surfactant protein A (SP-A)

ES:24

<400> 28

Met Trp Leu Cys Pro Leu Ala Leu Thr Leu Ile Leu Met Ala Ala Ser
1 5 10 15

Gly Ala Ala Cys Glu Val Lys Asp Val Cys Val Gly Ser Pro Gly Ile
20 25 30

Pro Gly Thr Pro Gly Ser His Gly Leu Pro Gly Arg Asp Gly Arg Asp
35 40 45

Gly Val Lys Gly Asp Pro Gly Pro Pro Gly Pro Met Gly Pro Pro Gly
50 55 60

Glu Thr Pro Cys Pro Pro Gly Asn Asn Gly Leu Pro Gly Ala Pro Gly
65 70 75 80

Val Pro Gly Glu Arg Gly Glu Lys Gly Glu Pro Gly Glu Arg Gly Pro
85 90 95

Pro Gly Leu Pro Ala His Leu Asp Glu Glu Leu Gln Ala Thr Leu His
100 105 110

Asp Phe Arg His Gln Ile Leu Gln Thr Arg Gly Ala Leu Ser Leu Gln
115 120 125

Gly Ser Ile Met Thr Val Gly Glu Lys Val Phe Ser Ser Asn Gly Gln
130 135 140

Ser Ile Thr Phe Asp Ala Ile Gln Glu Ala Cys Ala Arg Ala Gly Gly
145 150 155 160

Arg Ile Ala Val Pro Arg Asn Pro Glu Glu Asn Glu Ala Ile Ala Ser
165 170 175

Phe Val Lys Lys Tyr Asn Thr Tyr Ala Tyr Val Gly Leu Thr Glu Gly
 180 185 190

Pro Ser Pro Gly Asp Phe Arg Tyr Ser Asp Gly Thr Pro Val Asn Tyr
 195 200 205

Thr Asn Trp Tyr Arg Gly Glu Pro Ala Gly Arg Gly Lys Glu Gln Cys
 210 215 220

Val Glu Met Tyr Thr Asp Gly Gln Trp Asn Asp Arg Asn Cys Leu Tyr
 225 230 235 240

Ser Arg Leu Thr Ile Cys Glu Phe
 245

<210> 29
 <211> 375
 <212> PRT
 <213> Homo sapiens

<220>
 <223> surfactant protein D (SP-D)

<400> 29
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 1 5 10 15

Gly Tyr Leu Glu Ala Glu Met Lys Thr Tyr Ser His Arg Thr Thr Pro
 20 25 30

Ser Ala Cys Thr Leu Val Met Cys Ser Ser Val Glu Ser Gly Leu Pro
 35 40 45

Gly Arg Asp Gly Arg Asp Gly Arg Glu Gly Pro Arg Gly Glu Lys Gly
 50 55 60

Asp Pro Gly Leu Pro Gly Ala Ala Gly Gln Ala Gly Met Pro Gly Gln
 65 70 75 80

Ala Gly Pro Val Gly Pro Lys Gly Asp Asn Gly Ser Val Gly Glu Pro
 85 90 95

Gly Pro Lys Gly Asp Thr Gly Pro Ser Gly Pro Pro Gly Pro Pro Gly
 100 105 110

Val Pro Gly Pro Ala Gly Arg Glu Gly Pro Leu Gly Lys Gln Gly Asn
 115 120 125

Ile Gly Pro Gln Gly Lys Pro Gly Pro Lys Gly Glu Ala Gly Pro Lys
 130 135 140

Gly Glu Val Gly Ala Pro Gly Met Gln Gly Ser Ala Gly Ala Arg Gly
 145 150 155 160

Leu Ala Gly Pro Lys Gly Glu Arg Gly Val Pro Gly Glu Arg Gly Val
165 170 175

Pro Gly Asn Ala Gly Ala Ala Gly Ser Ala Gly Ala Met Gly Pro Gln
180 185 190

Gly Ser Pro Gly Ala Arg Gly Pro Pro Gly Leu Lys Gly Asp Lys Gly
195 200 205

Ile Pro Gly Asp Lys Gly Ala Lys Gly Glu Ser Gly Leu Pro Asp Val
210 215 220

Ala Ser Leu Arg Gln Gln Val Glu Ala Leu Gln Gly Gln Val Gln His
225 230 235 240

Leu Gln Ala Ala Phe Ser Gln Tyr Lys Lys Val Glu Leu Phe Pro Asn
245 250 255

Gly Gln Ser Val Gly Glu Lys Ile Phe Lys Thr Ala Gly Phe Val Lys
260 265 270

Pro Phe Thr Glu Ala Gln Leu Leu Cys Thr Gln Ala Gly Gly Gln Leu
275 280 285

Ala Ser Pro Arg Ser Ala Ala Glu Asn Ala Ala Leu Gln Gln Leu Val
290 295 300

Val Ala Lys Asn Glu Ala Ala Phe Leu Ser Met Thr Asp Ser Lys Thr
305 310 315 320

Glu Gly Lys Phe Thr Tyr Pro Thr Gly Glu Ser Leu Val Tyr Ser Asn
325 330 335

Trp Ala Pro Gly Glu Pro Asn Asp Asp Gly Gly Ser Glu Asp Cys Val
340 345 350

Glu Ile Phe Thr Asn Gly Lys Trp Asn Asp Arg Ala Cys Gly Glu Lys
355 360 365

Arg Leu Val Val Cys Glu Phe
370 375